

SCORE Search Results Details for Application 10649457 and Search Result us-10-649-457-1.rge.

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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 18:30:39 ; Search time 12859 Seconds
(without alignments)
11412.966 Million cell updates/sec

Title: US-10-649-457-1
Perfect score: 2295
Sequence: 1 atgaagaagcgcaagggtgct.....agggctacgagatcggctaa 2295

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	1587.2	69.2	2208	2	CS249839	CS249839 Sequence
2	1587.2	69.2	2211	2	CS249845	CS249845 Sequence
3	1493.2	65.1	2228	2	AX353770	AX353770 Sequence
4	1430.2	62.3	2277	8	AY428556	AY428556 Synthetic
5	1328.4	57.9	2202	2	CS061690	CS061690 Sequence
6	1247	54.3	2369	15	AF306779	AF306779 Bacillus
7	1247	54.3	2549	15	AF268967	AF268967 Bacillus
8	1245.4	54.3	2295	2	CS135651	CS135651 Sequence
9	1245.4	54.3	2295	2	CS176591	CS176591 Sequence
10	1245.4	54.3	2295	2	CS185124	CS185124 Sequence
11	1245.4	54.3	2295	15	AY997299	AY997299 Bacillus
12	1245.4	54.3	2369	15	AF306778	AF306778 Bacillus
13	1245.4	54.3	2369	15	AF306782	AF306782 Bacillus
c 14	1245.4	54.3	181654	15	AF065404	AF065404 Bacillus
15	1245.4	54.3	181677	15	AE011190	AE011190 Bacillus
16	1245.4	54.3	181677	15	AE017336	AE017336 Bacillus
17	1243.8	54.2	2295	2	CS176595	CS176595 Sequence
18	1243.8	54.2	2369	15	AF306780	AF306780 Bacillus
19	1243.8	54.2	2369	15	AF306781	AF306781 Bacillus
20	1243.8	54.2	2369	15	AF306783	AF306783 Bacillus
21	1243.8	54.2	2605	2	AX933603	AX933603 Sequence
22	1243.8	54.2	4235	2	I33396	I33396 Sequence 3
23	1243.8	54.2	4235	2	I69374	I69374 Sequence 3
24	1243.8	54.2	4235	15	BACPAG	M22589 Bacillus an
25	1242.2	54.1	2295	2	CS176599	CS176599 Sequence
26	1240.6	54.1	2295	2	AR570594	AR570594 Sequence
27	1218.4	53.1	2304	2	CS176593	CS176593 Sequence
28	1217	53.0	2307	2	CS176597	CS176597 Sequence
29	1216.8	53.0	2304	2	CS176581	CS176581 Sequence
30	1215.2	52.9	2304	2	CS176589	CS176589 Sequence
31	1213.8	52.9	2307	2	CS176583	CS176583 Sequence
32	1213.8	52.9	2307	2	CS176585	CS176585 Sequence
33	1213.8	52.9	2307	2	CS176587	CS176587 Sequence
34	1209.6	52.7	2292	2	AR570596	AR570596 Sequence
35	1207.6	52.6	2231	15	BAN413936	AJ413936 Bacillus
36	1207.4	52.6	2225	15	BAN413937	AJ413937 Bacillus
37	1198.4	52.2	2208	2	CS135652	CS135652 Sequence
38	1198.4	52.2	2208	2	CS249840	CS249840 Sequence
39	1198.4	52.2	2211	2	CS061689	CS061689 Sequence
40	1198.4	52.2	2211	2	CS249846	CS249846 Sequence
41	1198	52.2	2227	15	AY700758	AY700758 Bacillus
42	1196.8	52.1	2208	2	AX353783	AX353783 Sequence
43	1196.8	52.1	2211	2	AR570595	AR570595 Sequence
44	1174.4	51.2	2709	2	I33400	I33400 Sequence 11
45	1174.4	51.2	2709	2	I69378	I69378 Sequence 11

ALIGNMENTS

RESULT 1

CS249839

LOCUS CS249839 2208 bp DNA linear PAT 18-JAN-2006

DEFINITION Sequence 1 from Patent WO2005123764.

ACCESSION CS249839

VERSION CS249839.1 GI:85362418

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Brehm,J.

TITLE Preparation of protective antigen from bacillus anthracis

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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 18:24:58 ; Search time 1418 Seconds
(without alignments)
11284.422 Million cell updates/sec

Title: US-10-649-457-1
Perfect score: 2295
Sequence: 1 atgaagaagcgcaagggtgct.....agggtctacgagatcggctaa 2295

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: geneseqn2001as:*
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- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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3	1587.2	69.2	2208	15	AEF05327	Aef05327 DNA encod
4	1587.2	69.2	2211	15	AEF05333	Aef05333 DNA encod
5	1543.8	67.3	2268	12	ADL28550	Adi28550 Bacillus
6	1526.2	66.5	2292	12	ADL72890	Adl72890 Anthrax v
7	1519	66.2	2295	12	ADL72888	Adl72888 Anthrax v
8	1505.4	65.6	2292	12	ADL72889	Adl72889 Anthrax v
9	1493.2	65.1	2228	6	AAD29115	Aad29115 Bacillus
10	1430.2	62.3	2277	12	ADL72872	Adl72872 Anthrax v
11	1430.2	62.3	6425	15	AEE68484	Aee68484 VR6307 ex
12	1328.4	57.9	2202	14	ADY84836	Ady84836 Bacillus
13	1245.4	54.3	2295	14	ADW29247	Adw29247 B. anthra
14	1245.4	54.3	2295	14	AEB63728	Aeb63728 DNA encod
15	1245.4	54.3	2295	14	AED17611	Aed17611 Anthrax t
16	1245.4	54.3	2295	14	AED25935	Aed25935 Bacillus
17	1245.4	54.3	2295	14	AED29267	Aed29267 Primer fo
18	1245.4	54.3	8198	12	ADL16342	Adl16342 pBP103 ex
19	1245.4	54.3	9286	12	ADL16345	Adl16345 pBP105 ex
20	1243.8	54.2	2295	3	AAZ56874	Aaz56874 B. anthra
21	1243.8	54.2	2295	4	AAC86016	Aac86016 Wild type
22	1243.8	54.2	2295	14	AED17615	Aed17615 Anthrax t
23	1243.8	54.2	2605	10	ADE65871	Ade65871 Bacillus
24	1243.8	54.2	2605	14	AEB20797	Aeb20797 Bacillus
25	1243.8	54.2	4235	2	AAQ70180	Aaq70180 Sequence
26	1243.8	54.2	4235	10	ACF58207	Acf58207 B. anthrac
27	1243.8	54.2	4235	12	ADL72868	Adl72868 Anthrax v
28	1242.2	54.1	2295	14	AED17619	Aed17619 Anthrax t
29	1218.4	53.1	2304	14	AED17613	Aed17613 Anthrax t
30	1217	53.0	2307	14	AED17617	Aed17617 Anthrax t
31	1216.8	53.0	2304	14	AED17601	Aed17601 Anthrax t
32	1215.2	52.9	2304	14	AED17609	Aed17609 Anthrax t
33	1213.8	52.9	2307	14	AED17603	Aed17603 Anthrax t
34	1213.8	52.9	2307	14	AED17605	Aed17605 Anthrax t
35	1213.8	52.9	2307	14	AED17607	Aed17607 Anthrax t
36	1209.6	52.7	2292	3	AAZ56876	Aaz56876 B. anthra
37	1198.4	52.2	2208	12	ADL16343	Adl16343 Bacillus
38	1198.4	52.2	2208	12	ADL16346	Adl16346 Bacillus
39	1198.4	52.2	2208	14	AEB63729	Aeb63729 DNA encod
40	1198.4	52.2	2208	15	AEF05328	Aef05328 DNA encod
41	1198.4	52.2	2211	14	ADY84835	Ady84835 Bacillus
42	1198.4	52.2	2211	15	AEF05334	Aef05334 DNA encod
43	1196.8	52.1	2208	6	AAD29121	Aad29121 Bacillus
44	1196.8	52.1	2208	6	AAI99904	Aai99904 Anthrax P
45	1196.8	52.1	2208	14	ADW05484	Adw05484 B. anthra

ALIGNMENTS

RESULT 1

AEF06482

ID AEF06482 standard; DNA; 2295 BP.

XX

AC AEF06482;

XX

DT 23-MAR-2006 (first entry)

XX

DE Humanized protective antigen coding sequence, SEQ ID 1.

XX

KW Antibacterial; Vaccine; protective antigen; gene; ds.

XX

OS Synthetic.

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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 18:35:43 ; Search time 429 Seconds
(without alignments)
10009.778 Million cell updates/sec

Title: US-10-649-457-1
Perfect score: 2295
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/8_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1243.8	54.2	4235	2	US-08-021-601-3 Sequence 3, Appli
2	1243.8	54.2	4235	2	US-08-082-849B-3 Sequence 3, Appli
3	1243.8	54.2	4235	7	PCT-US94-01624-3 Sequence 3, Appli

4	1240.6	54.1	2295	3	US-09-350-729A-1	Sequence 1, Appli
5	1209.6	52.7	2292	3	US-09-350-729A-3	Sequence 3, Appli
6	1196.8	52.1	2211	3	US-09-350-729A-2	Sequence 2, Appli
7	1174.4	51.2	2709	2	US-08-021-601-11	Sequence 11, Appl
8	1174.4	51.2	2709	2	US-08-082-849B-11	Sequence 11, Appl
9	1174.4	51.2	2709	7	PCT-US94-01624-11	Sequence 11, Appl
10	1064	46.4	2160	2	US-08-082-849B-30	Sequence 30, Appl
11	1064	46.4	2160	7	PCT-US94-01624-30	Sequence 30, Appl
12	923	40.2	1710	3	US-09-350-729A-4	Sequence 4, Appli
13	404.8	17.6	867	3	US-09-273-839A-7	Sequence 7, Appli
14	351.2	15.3	2655	2	US-08-471-033-17	Sequence 17, Appl
15	351.2	15.3	2655	2	US-08-471-044-17	Sequence 17, Appl
16	351.2	15.3	2655	2	US-08-463-483A-17	Sequence 17, Appl
17	351.2	15.3	2655	2	US-08-471-046A-17	Sequence 17, Appl
18	351.2	15.3	2655	2	US-08-470-566B-17	Sequence 17, Appl
19	351.2	15.3	2655	2	US-08-469-334-17	Sequence 17, Appl
20	351.2	15.3	2655	3	US-09-300-529-17	Sequence 17, Appl
21	348	15.2	2655	2	US-08-471-033-26	Sequence 26, Appl
22	348	15.2	2655	2	US-08-471-044-26	Sequence 26, Appl
23	348	15.2	2655	2	US-08-463-483A-26	Sequence 26, Appl
24	348	15.2	2655	2	US-08-471-046A-26	Sequence 26, Appl
25	348	15.2	2655	2	US-08-470-566B-26	Sequence 26, Appl
26	348	15.2	2655	2	US-08-469-334-26	Sequence 26, Appl
27	348	15.2	2655	3	US-09-300-529-26	Sequence 26, Appl
28	344	15.0	2576	2	US-08-471-033-35	Sequence 35, Appl
29	344	15.0	2576	2	US-08-471-044-35	Sequence 35, Appl
30	344	15.0	2576	2	US-08-463-483A-35	Sequence 35, Appl
31	344	15.0	2576	2	US-08-471-046A-35	Sequence 35, Appl
32	344	15.0	2576	2	US-08-470-566B-35	Sequence 35, Appl
33	344	15.0	2576	2	US-08-469-334-35	Sequence 35, Appl
34	344	15.0	2576	3	US-09-300-529-35	Sequence 35, Appl
35	344	15.0	4031	2	US-08-471-033-49	Sequence 49, Appl
36	344	15.0	4031	2	US-08-471-044-49	Sequence 49, Appl
37	344	15.0	4031	2	US-08-463-483A-49	Sequence 49, Appl
38	344	15.0	4031	2	US-08-471-046A-49	Sequence 49, Appl
39	344	15.0	4031	2	US-08-470-566B-49	Sequence 49, Appl
40	344	15.0	4031	2	US-08-469-334-49	Sequence 49, Appl
41	344	15.0	4031	3	US-09-300-529-49	Sequence 49, Appl
42	279	12.2	2004	2	US-08-471-033-18	Sequence 18, Appl
43	279	12.2	2004	2	US-08-471-044-18	Sequence 18, Appl
44	279	12.2	2004	2	US-08-463-483A-18	Sequence 18, Appl
45	279	12.2	2004	2	US-08-471-046A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-08-021-601-3

; Sequence 3, Application US/08021601

; Patent No. 5591631

; GENERAL INFORMATION:

; APPLICANT: Leppla, Stephen H.

; APPLICANT: Klimpel, Kurt R.

; APPLICANT: Nichols, Peter J.

; APPLICANT: Arora, Naveen

; APPLICANT: Singh, Yogendra

; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND

; TITLE OF INVENTION: RELATED METHODS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Needle & Rosenberg, P.C.

; STREET: 133 Carnegie Way, Suite 400

; CITY: Atlanta

; STATE: Georgia

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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 18:34:11 ; Search time 10751 Seconds
(without alignments)
11937.017 Million cell updates/sec

Title: US-10-649-457-1
Perfect score: 2295
Sequence: 1 atgaagaagcgcaaggcgct.....agggctacgagatcggctaa 2295

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: gb_est4:*
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- 5: gb_est6:*
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- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	IDB	Description
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c	3	99.2	4.3	889	5	CK159613	CK159613 FGAS04107
	4	94.6	4.1	584	14	DE225508	DE225508 Trifolium
	5	92.4	4.0	1071	10	DW613958	DW613958 CLJ277-H0
	6	92.4	4.0	1941	13	CL971508	CL971508 OsIFCC021
	7	92	4.0	515	14	DE229111	DE229111 Trifolium
	8	92	4.0	1017	14	DU732166	DU732166 APKF1595
	9	91.6	4.0	2598	6	AY103647	AY103647 Zea mays
	10	91	4.0	527	12	CE480293	CE480293 tigr-gss-
	11	91	4.0	584	14	DE214541	DE214541 Trifolium
	12	91	4.0	1933	6	AY325173	AY325173 Rattus no
	13	89.8	3.9	3317	6	BC039313	BC039313 Homo sapi
	14	89.6	3.9	547	14	DE229299	DE229299 Trifolium
	15	89.6	3.9	1707	13	CL969422	CL969422 OsIFCC040
	16	89.6	3.9	1962	13	CL961326	CL961326 OsIFCC005
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c	20	86.6	3.8	1029	14	DU734977	DU734977 APKF3021
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	22	85.4	3.7	777	5	CK809576	CK809576 Rasgsc322
	23	85.2	3.7	2773	6	AK171820	AK171820 Mus muscu
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	26	83.8	3.7	789	11	BZ115869	BZ115869 CH230-255
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	28	83	3.6	658	3	BW265514	BW265514 BW265514
	29	83	3.6	663	3	BW259047	BW259047 BW259047
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	34	82.4	3.6	2529	13	CL964961	CL964961 OsIFCC011
	35	81.8	3.6	581	5	CF569196	CF569196 EST057 Su
	36	81.4	3.5	2775	6	AK159139	AK159139 Mus muscu
	37	80.6	3.5	593	9	DN606897	DN606897 EST02108
	38	80.6	3.5	1132	10	DW042205	DW042205 CFW300-E0
	39	80.4	3.5	687	9	DN470309	DN470309 USDA-FP_1
	40	80.2	3.5	2475	13	CL970193	CL970193 OsIFCC019
	41	79.8	3.5	869	9	DN413386	DN413386 LIB4215-0
	42	79.4	3.5	1575	13	CL979927	CL979927 OsIFCC045
	43	79.2	3.5	519	14	DE229747	DE229747 Trifolium
	44	79.2	3.5	714	13	CL855158	CL855158 OR_CBa008
	45	79.2	3.5	969	6	AY383694	AY383694 Rattus no

ALIGNMENTS

RESULT 1

CK159167/c

LOCUS CK159167 869 bp mRNA linear EST 05-DEC-2003

DEFINITION FGAS040564 Triticum aestivum FGAS: TaLT5 Triticum aestivum cDNA, mRNA sequence.

ACCESSION CK159167

VERSION CK159167.1 GI:38985053

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Pooideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 869)